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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/845,335

DATE: 12/26/2001

TIME: 15:50:36

Input Set : N:\Crf3\RULE60\09845335.raw
Output Set: N:\CRF3\12262001\I845335.raw

1 <110> APPLICANT: CLOUGH, BARBARA
2 PREISER, PETER
3 WILSON, ROBERT
4 <120> TITLE OF INVENTION: AN EF-TU PROTEIN ENCODED ON THE PLASTID DNA OF THE
5 MALARIA PARASITE AND PROTEIN SYNTHESIS INHIBITORS
6 EFFECTIVE AS ANTI-MALARIAL COMPOUNDS
7 <130> FILE REFERENCE: N68837B GCW PJC DP
8 <140> CURRENT APPLICATION NUMBER: 09/845,335
9 <141> CURRENT FILING DATE: 2001-12-26
10 <150> PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/140,466
W--> 11 <151> PRIOR FILING DATE: EARLIER FILING DATE: 1998-08-26
12 <160> NUMBER OF SEQ ID NOS: 14
13 <170> SOFTWARE: PatentIn Ver. 2.1
15 <210> SEQ ID NO: 1
16 <211> LENGTH: 1230
17 <212> TYPE: DNA
18 <213> ORGANISM: Plasmodium falciparum
19 <220> FEATURE:
20 <221> NAME/KEY: CDS
21 <222> LOCATION: (1)..(1230)
22 <400> SEQUENCE: 1
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25 1 5 10 15
26 act ata ggg cat gta gat cat gga aaa act aca tta aca aca gct ata 96
27 Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ile
28 20 25 30
29 tct tat tta tta aat tta caa gga tta tca aaa aaa tat aat tat tca 144
30 Ser Tyr Leu Leu Asn Leu Gln Gly Leu Ser Lys Lys Tyr Asn Tyr Ser
31 35 40 45
32 gat att gat tca gct cca gaa gaa aaa ata aga ggt att aca ata aat 192
33 Asp Ile Asp Ser Ala Pro Glu Glu Lys Ile Arg Gly Ile Thr Ile Asn
34 50 55 60
35 aca aca cat att gaa tat gaa act tta aca aaa cat tgt gct cat ata 240
36 Thr Thr His Ile Glu Tyr Glu Thr Leu Thr Lys His Cys Ala His Ile
37 65 70 75 80
38 gat tgt cca gga cat tcc gat tat att aaa aat atg att ata gga gcc 288
39 Asp Cys Pro Gly His Ser Asp Tyr Ile Lys Asn Met Ile Ile Gly Ala
40 85 90 95
41 aca caa atg gat ata gca att tta gta ata tct ata ata gat ggt ata 336
42 Thr Gln Met Asp Ile Ala Ile Leu Val Ile Ser Ile Ile Asp Gly Ile
43 100 105 110
44 atg cct caa act tat gaa cat tta tta ata aaa caa ata ggt ata 384
45 Met Pro Gln Thr Tyr Glu His Leu Leu Ile Lys Gln Ile Gly Ile
46 115 120 125
47 aaa aat ata att att ttt tta aat aaa gaa gat tta tgt gat gat gtt 432
48 Lys Asn Ile Ile Phe Leu Asn Lys Glu Asp Leu Cys Asp Asp Val

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49	130	135	140	
50	gaa tta ata gat ttt ata aaa tta gaa gta aat gaa tta tta att aaa			480
51	Glu Leu Ile Asp Phe Ile Lys Leu Glu Val Asn Glu Leu Leu Ile Lys			
52	145 150 155 160			
53	tat aat ttt gat tta aat tat ata cat ata tta act ggt tca gca tta			528
54	Tyr Asn Phe Asp Leu Asn Tyr Ile His Ile Leu Thr Gly Ser Ala Leu			
55	165 170 175			
56	aat gta ata aat ata att caa aaa aat aag gat tat gaa tta ata aaa			576
57	Asn Val Ile Asn Ile Ile Gln Lys Asn Lys Asp Tyr Glu Leu Ile Lys			
58	180 185 190			
59	tct aat att tgg ata caa aaa tta aat aat tta att caa ata att gat			624
60	Ser Asn Ile Trp Ile Gln Lys Leu Asn Asn Leu Ile Gln Ile Ile Asp			
61	195 200 205			
62	aat att ata ata cct act aga aaa att aat gat tac ttt tta atg tca			672
63	Asn Ile Ile Ile Pro Thr Arg Lys Ile Asn Asp Tyr Phe Leu Met Ser			
64	210 215 220			
65	ata gaa gat gta ttt tct ata aca ggt aga ggt aca gta gta aca ggt			720
66	Ile Glu Asp Val Phe Ser Ile Thr Gly Arg Gly Thr Val Val Thr Gly			
67	225 230 235 240			
68	aag att gaa caa gga tgt ata aat tta aat gat gaa att gaa att tta			768
69	Lys Ile Glu Gln Gly Cys Ile Asn Leu Asn Asp Glu Ile Glu Ile Leu			
70	245 250 255			
71	aaa ttt gaa aaa tca tct cct aat tta aca aca gtt ata gga tta gaa			816
72	Lys Phe Glu Lys Ser Ser Pro Asn Leu Thr Thr Val Ile Gly Leu Glu			
73	260 265 270			
74	atg ttt aaa aaa caa tta aca caa gca caa tcc gga gat aat gta ggt			864
75	Met Phe Lys Lys Gln Leu Thr Gln Ala Gln Ser Gly Asp Asn Val Gly			
76	275 280 285			
77	att tta tta aga aat att caa aaa aat gat ata aat aga ggt atg att			912
78	Ile Leu Leu Arg Asn Ile Gln Lys Lys Asp Ile Lys Arg Gly Met Ile			
79	290 295 300			
80	tta gca aca cct aat aaa tta aaa gta tat aag tct ttt ata gct gaa			960
81	Leu Ala Thr Pro Asn Lys Leu Lys Val Tyr Lys Ser Phe Ile Ala Glu			
82	305 310 315 320			
83	aca tat att tta act aaa gaa gaa ggt ggt cgt cat aaa cct ttt aat			1008
84	Thr Tyr Ile Leu Thr Lys Glu Glu Gly Arg His Lys Pro Phe Asn			
85	325 330 335			
86	att gga tat aaa cct caa ttt ttt att cgt aca gta gat gtt act gga			1056
87	Ile Gly Tyr Lys Pro Gln Phe Phe Ile Arg Thr Val Asp Val Thr Gly			
88	340 345 350			
89	gaa att aaa aat ata tat tta aat gaa aat gta caa aaa gta gct ata			1104
90	Glu Ile Lys Asn Ile Tyr Leu Asn Glu Asn Val Gln Lys Val Ala Ile			
91	355 360 365			
92	cct gga gat aaa ata aca tta cat att gaa tta aaa cat tat ata gtg			1152
93	Pro Gly Asp Lys Ile Thr Leu His Ile Glu Leu Lys His Tyr Ile Val			
94	370 375 380			
95	ttg aca tta aat atg aaa ttt tct att aga gaa gga gga aaa aca ata			1200
96	Leu Thr Leu Asn Met Lys Phe Ser Ile Arg Glu Gly Gly Lys Thr Ile			
97	385 390 395 400			

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100 405 410
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104 <212> TYPE: PRT
105 <213> ORGANISM: Plasmodium falciparum
106 <400> SEQUENCE: 2
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109 Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ile
110 20 25 30
111 Ser Tyr Leu Leu Asn Leu Gln Gly Leu Ser Lys Lys Tyr Asn Tyr Ser
112 35 40 45
113 Asp Ile Asp Ser Ala Pro Glu Glu Lys Ile Arg Gly Ile Thr Ile Asn
114 50 55 60
115 Thr Thr His Ile Glu Tyr Glu Thr Leu Thr Lys His Cys Ala His Ile
116 65 70 75 80
117 Asp Cys Pro Gly His Ser Asp Tyr Ile Lys Asn Met Ile Ile Gly Ala
118 85 90 95
119 Thr Gln Met Asp Ile Ala Ile Leu Val Ile Ser Ile Ile Asp Gly Ile
120 100 105 110
121 Met Pro Gln Thr Tyr Glu His Leu Leu Ile Lys Gln Ile Gly Ile
122 115 120 125
123 Lys Asn Ile Ile Ile Phe Leu Asn Lys Glu Asp Leu Cys Asp Asp Val
124 130 135 140
125 Glu Leu Ile Asp Phe Ile Lys Leu Glu Val Asn Glu Leu Leu Ile Lys
126 145 150 155 160
127 Tyr Asn Phe Asp Leu Asn Tyr Ile His Ile Leu Thr Gly Ser Ala Leu
128 165 170 175
129 Asn Val Ile Asn Ile Ile Gln Lys Asn Lys Asp Tyr Glu Leu Ile Lys
130 180 185 190
131 Ser Asn Ile Trp Ile Gln Lys Leu Asn Asn Leu Ile Gln Ile Ile Asp
132 195 200 205
133 Asn Ile Ile Ile Pro Thr Arg Lys Ile Asn Asp Tyr Phe Leu Met Ser
134 210 215 220
135 Ile Glu Asp Val Phe Ser Ile Thr Gly Arg Gly Thr Val Val Thr Gly
136 225 230 235 240
137 Lys Ile Glu Gln Gly Cys Ile Asn Leu Asn Asp Glu Ile Glu Ile Leu
138 245 250 255
139 Lys Phe Glu Lys Ser Ser Pro Asn Leu Thr Thr Val Ile Gly Leu Glu
140 260 265 270
141 Met Phe Lys Lys Gln Leu Thr Gln Ala Gln Ser Gly Asp Asn Val Gly
142 275 280 285
143 Ile Leu Leu Arg Asn Ile Gln Lys Lys Asp Ile Lys Arg Gly Met Ile
144 290 295 300
145 Leu Ala Thr Pro Asn Lys Leu Lys Val Tyr Lys Ser Phe Ile Ala Glu
146 305 310 315 320
147 Thr Tyr Ile Leu Thr Lys Glu Glu Gly Arg His Lys Pro Phe Asn

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148 325 330 335
 149 Ile Gly Tyr Lys Pro Gln Phe Phe Ile Arg Thr Val Asp Val Thr Gly
 150 340 345 350
 151 Glu Ile Lys Asn Ile Tyr Leu Asn Glu Asn Val Gln Lys Val Ala Ile
 152 355 360 365
 153 Pro Gly Asp Lys Ile Thr Leu His Ile Glu Leu Lys His Tyr Ile Val
 154 370 375 380
 155 Leu Thr Leu Asn Met Lys Phe Ser Ile Arg Glu Gly Gly Lys Thr Ile
 156 385 390 395 400
 157 Gly Ala Gly Ile Ile Thr Glu Ile Lys Asn
 158 405 410
 160 <210> SEQ ID NO: 3
 161 <211> LENGTH: 409
 162 <212> TYPE: PRT
 163 <213> ORGANISM: Anacystis nidulans
 164 <400> SEQUENCE: 3
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 167 Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
 168 20 25 30
 169 Thr Thr Val Leu Ala Lys Ala Gly Met Ala Lys Ala Arg Ala Tyr Ala
 170 35 40 45
 171 Asp Ile Asp Ala Ala Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn
 172 50 55 60
 173 Thr Ala His Val Glu Tyr Glu Thr Gly His Arg His Tyr Ala His Val
 174 65 70 75 80
 175 Asp Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala
 176 85 90 95
 177 Ala Gln Met Asp Gly Ala Ile Leu Val Val Ser Ala Ala Asp Gly Pro
 178 100 105 110
 179 Met Pro Gln Thr Arg Glu His Ile Leu Leu Ala Lys Gln Val Gly Val
 180 115 120 125
 181 Pro Asn Ile Val Val Phe Leu Asn Lys Glu Asp Met Val Asp Asp Ala
 182 130 135 140
 183 Glu Leu Leu Glu Leu Val Glu Leu Glu Val Arg Glu Leu Leu Ser Ser
 184 145 150 155 160
 185 Tyr Asp Phe Pro Gly Asp Asp Ile Pro Ile Val Ala Gly Ser Ala Leu
 186 165 170 175
 187 Gln Ala Leu Glu Ala Ile Gln Gly Gly Ala Ser Gly Gln Lys Gly Asp
 188 180 185 190
 189 Asn Pro Trp Val Asp Lys Ile Leu Lys Leu Met Glu Glu Val Asp Ala
 190 195 200 205
 191 Tyr Ile Pro Thr Pro Glu Arg Glu Val Asp Arg Pro Phe Leu Met Ala
 192 210 215 220
 193 Val Glu Asp Val Phe Thr Ile Thr Gly Arg Gly Thr Val Ala Thr Gly
 194 225 230 235 240
 195 Arg Ile Glu Arg Gly Ser Val Lys Val Gly Glu Thr Ile Glu Ile Val
 196 245 250 255
 197 Gly Leu Arg Asp Thr Arg Ser Thr Thr Val Thr Gly Val Glu Met Phe

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198 260 265 270
 199 Gln Lys Thr Leu Asp Glu Gly Leu Ala Gly Asp Asn Val Gly Leu Leu
 200 275 280 285
 201 Leu Arg Gly Ile Gln Lys Thr Asp Ile Glu Arg Gly Met Val Leu Ala
 202 290 295 300
 203 Lys Pro Gly Ser Ile Thr Pro His Thr Lys Phe Glu Ser Glu Val Tyr
 204 305 310 315 320
 205 Val Leu Lys Lys Glu Glu Gly Gly Arg His Thr Pro Phe Phe Pro Gly
 206 325 330 335
 207 Tyr Arg Pro Gln Phe Tyr Val Arg Thr Thr Asp Val Thr Gly Ala Ile
 208 340 345 350
 209 Ser Asp Phe Thr Ala Asp Asp Gly Ser Ala Ala Glu Met Val Ile Pro
 210 355 360 365
 211 Gly Asp Arg Ile Lys Met Thr Val Glu Leu Ile Asn Pro Ile Ala Ile
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 213 Glu Gln Gly Met Arg Phe Ala Ile Arg Glu Gly Gly Arg Thr Ile Gly
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 219 <211> LENGTH: 408
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 221 <213> ORGANISM: Cryptomonas phi
 222 <400> SEQUENCE: 4
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 225 Thr Ile Gly His Val Asp His Gly Lys Thr Thr Leu Thr Ala Ala Ile
 226 20 25 30
 227 Ser Ala Thr Leu Ser Gln Tyr Thr Gly Lys Ser Lys Lys Phe Asp Glu
 228 35 40 45
 229 Ile Asp Ser Ala Pro Glu Glu Lys Ala Arg Gly Ile Thr Ile Asn Thr
 230 50 55 60
 231 Ala His Val Glu Tyr Glu Thr Asp Lys Trp Tyr Tyr Ala His Val Asp
 232 65 70 75 80
 233 Cys Pro Gly His Ala Asp Tyr Val Lys Asn Met Ile Thr Gly Ala Ala
 234 85 90 95
 235 Gln Met Asp Gly Ala Ile Leu Val Cys Ser Ala Ala Asn Gly Pro Met
 236 100 105 110
 237 Pro Gln Thr Arg Glu His Ile Leu Ala Lys Gln Val Gly Val Pro
 238 115 120 125
 239 Tyr Ile Val Val Phe Leu Asn Lys Ala Asp Met Val Asp Asp Glu Glu
 240 130 135 140
 241 Leu Leu Glu Leu Val Gln Leu Glu Val Gln Glu Leu Leu Glu Lys Tyr
 242 145 150 155 160
 243 Asp Phe Pro Gly Ser Glu Ile Pro Phe Val Ala Gly Ser Ala Leu Leu
 244 165 170 175
 245 Ala Leu Glu Ala Val Ala Asn Asn Pro Thr Ile Lys Arg Gly Glu Asp
 246 180 185 190
 247 Lys Trp Val Asp Thr Ile Tyr Gln Leu Met Asp Lys Val Asp Glu Tyr

VERIFICATION SUMMARY

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